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10/769,514	01/30/2004	Anthony Bernard Schryvers	028722-376	8013

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EXAMINER

BASKAR, PADMAVATHI

ART UNIT	PAPER NUMBER
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1645

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	04/11/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary

Application No.

10/769,514

Applicant(s)

SCHRYVERS, ANTHONY
BERNARD

Examiner

Padmavathi v. Baskar

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 19 January 2007.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1,2,4, 5 and 8-27 is/are pending in the application.
- 4a) Of the above claim(s) 5 and 15-27 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1,2,4 and 8-14 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application
- 6) ☐ Other: _____

DETAILED ACTION

Amendment

1. Applicant's amendment filed on 1/19/07 is acknowledged.

Status of claims

2. Claims 3, 6 and 7 have been canceled.
Claims 1, 2, 4 and 8 have been amended
Claims 1,2, 4, and 8-14 under examination.
Claims 5 and 15-27 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected group of inventions and there being no allowable generic or linking claim.

Claim Rejections - 35 USC 112 maintained.

3. The rejection of claims 8-14 under 35 USC 112, first paragraph set forth in the previous action at page 8 is maintained .

Applicant argues that it would be routine in the art of immunology and molecular biology to generate an immune response in an animal using a polypeptide as defined in claim 1 in a vaccine . Subsequently challenging the animal with a Gram negative infection would also be routine. One skilled in the art could produce a polypeptide that can elicit an immune response from an animal using the present specification coupled with standard immunological techniques known in the art without undue experimentation.

The argument has been considered but has not been found persuasive because the claims are drawn to a vaccine composition and for the reasons set forth PREVIOUSLY the specification does not enable the breadth of the claims.

New Claim Rejections - 35 USC 112 based on the amendment.

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying.

5. Claims 1, 2, 4 and 8-14 are under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicant is referred to the revised guidelines on written description available at www.uspto.gov (O.G. published January 30, 2001). This is a written description rejection.

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Claims are drawn to an isolated polypeptide selected from the group consisting of:

b) a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions; and

c) a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus, wherein the polypeptide binds to a region of transferrin that is recognized by a bacterial transferrin binding protein B (TbpB), wherein the polypeptide molecule is an antibody, wherein the transferrin is human transferrin, and the transferrin binding protein is a transferrin binding protein B (TbpB) from a human Gram negative bacterial pathogen (These are considered as variants of SEQ.ID.NO:17) Claims are also drawn to a vaccine comprising said polypeptide vaccine capable of eliciting antibodies that recognize a plurality of different transferrin binding proteins, said antibodies that recognize at least two transferrin binding proteins of Gram negative bacteria or that recognize at least two transferrin binding proteins selected from the group consisting of transferrin binding proteins of *Neisseria* spp., *Haemophilus* spp., *Moraxella* spp., *Mannheimia* (*Pasteurella*) spp., *Actinobacillus* spp., and *Staphylococcus* spp or antibodies that recognize the transferrin binding proteins recognize *N. meningitidis*, *H. influenzae*, *M. catarrhalis* and *S. pneumoniae* or antibodies that recognize the transferrin binding proteins of *H. influenzae* and *M. catarrhalis* or antibodies that recognize the transferrin binding proteins of *N. meningitidis* and *H. influenzae*. Although drawn to DNA arts, the findings in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) and Enzo Biochem, Inc. V. Gen-Probe Inc. are relevant to the instant claims. The Federal Circuit addressed the application of the written description requirement to DNA-related inventions in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court stated that “[a] written description of an invention involving a chemical genus, like a description of a chemical species, ‘requires a precise definition, such as by structure, formula, [or] chemical name,’ of the claimed subject matter sufficient to distinguish it from other materials.” *Id.* At 1567, 43 USPQ2d at 1405. The court also stated that a generic statement such as “vertebrate insulin cDNA” or “mammalian insulin cDNA” without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. *Id.* At 1568, 43 USPQ2d at 1406. The court concluded that “naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material.” *Id.*

Finally, the court addressed the manner by which a genus of cDNAs might be described. “A description of a genus of cDNAs may be achieved by means of a recitation of a representative number

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of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." Id.

The Federal Circuit has recently clarified that a DNA molecule can be adequately described without disclosing its complete structure. See Enzo Biochem, Inc. V. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). The Enzo court adopted the standard that "the written description requirement can be met by 'show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristicsi.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics.'" Id. At 1324, 63 USPQ2d at 1613 (emphasis omitted, bracketed material in original). The inventions at issue in Lilly and Enzo were DNA constructs per se, the holdings of those cases are also applicable.

Thus, the instant specification may provide an adequate written description of a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus (considered as variants), wherein the polypeptide binds to a region of transferrin that is recognized by a bacterial transferrin binding protein B (TbpB) per Lilly by structurally describing a representative number of an isolated polypeptide variants of SEQ.ID.NO:17 "structural features common to the members of the genus, which features constitute a substantial portion of the genus." Alternatively, per Enzo, the specification can show that the claimed invention is complete "by disclosure of sufficiently detailed, relevant identifying characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

In this case, the specification does not disclose a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus, in a manner that satisfies either the Lilly or Enzo standards. The specification does not provide the complete structure of a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus nor does the specification provide any partial structure of a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus nor any physical or chemical characteristics of a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the

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amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino-terminus and/or carboxy-terminus nor any functional characteristics coupled with a known or disclosed correlation between structure and function. Although the specification discloses a single isolated polypeptide consisting of the amino acid sequence set forth as SEQ ID NO: 17, this does not provide a description of a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus that would satisfy the standard set out in Enzo.

The specification also fails to describe a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino-terminus and/or carboxy-terminus by the test set out in Lilly. The specification describes only a single isolated polypeptide consisting of the amino acid sequence set forth as SEQ ID NO: 17. Therefore, it necessarily fails to describe a "representative number" of such species. In addition, the specification also does not describe "structural features common to the members of the genus, which features constitute a substantial portion of the genus."

Thus, the specification does not provide an adequate written description of a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions and a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus that is required to practice the claimed invention.

Thus, the specification does not provide an adequate written description for variants of SEQ.ID.NO:17 Therefore claims 1, 2, 4 and 8-14 do not comply with 35 USC 112, first paragraph because it is not supported by an adequate written description in the specification.

6. Claims 1, 2, 4 and 8-14 (claim 8 depends from claim 1) are rejected under 35 USC 112, first paragraph because the specification, while enabling for an isolated polypeptide consisting of the amino acid sequence SEQ ID NO:17, wherein the polypeptide binds to a region of human transferrin that is recognized by a bacterial transferrin binding protein B (TbpB), said TbpB is from *M. catarrhalis* does not reasonably provide enablement for an isolated polypeptide selected from the group consisting of:

b) a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-5 conservative amino acid substitutions; and

c) a polypeptide consisting of the amino acid sequence of SEQ ID NO:17 and having 1-4 additional amino acid residues at the amino- terminus and/or carboxy-terminus, wherein the polypeptide binds to a region of transferrin that is recognized by a bacterial transferrin binding protein B (TbpB), wherein the polypeptide molecule is an antibody, wherein the transferrin is human transferrin, and the transferrin binding protein is a transferrin binding protein B (TbpB) from a human Gram negative bacterial pathogen

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(These are considered as variants of SEQ.ID.NO:17) The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Instant claims are evaluated for enablement using Wands analysis. Many of the factors regarding undue experimentation have been summarized in *In re Wands*, 858 F.2d 731, 8 USPQ2d 1400 (Fed.Circ.1988) as follows:

(1) the nature of the invention, (2) the state of the prior art, (3) the predictability or lack thereof in the art, (4) the amount of direction or guidance present, (5) the presence or absence of working examples, (6) the quantity of experimentation necessary, (7) the relative skill of those in the art, and (8) the breadth of the claims.

The specification teaches that the invention encompasses a molecule (e.g. peptide) which is capable of binding to a region of a transferrin protein (peptide region 1 of human transferrin) that is recognized by a bacterial transferrin binding protein especially peptides SEQ.ID.NO:15 or 16. The present amino acid sequence SEQ.ID.NO:17 represents overlap sequence of peptides SEQ.ID.NO:15 or 16, *Moraxella catarrhalis* transferrin binding protein. The specification suggests that the common amino acid sequence could be implicated as the recognition sequence (Table 2 and page 25). The specification teaches [0088] the truncation experiments, the N-lobe of *M. catarrhalis* was divided into seven segments with the identified binding peptides at their junctions. Segment 1 includes the amino acid sequence up to but not including binding region 1 (SEQ.ID.NO:15 or 16 or 17), segment 2 includes binding region 1 ((SEQ.ID.NO:15 or 16 or 17) and the amino acid sequence up to but not including binding region 2. The fusion proteins containing segments 1- 4 or less did not yield detectable binding activity in the solid-phase binding assay using the colorimetric substrate, chloronaphthol. In addition, if the truncations were probed with labeled hTf after SDS-PAGE and electro blotting, even the larger truncated proteins were not detected, similar to what was observed for the TbpB from *N. meningitidis*. The specification further teaches [0092] a potentially more sensitive means of detection that would not compromise the lifespan of the peptide libraries, HRP conjugates of the fusion proteins and a chemiluminescent system for detecting binding activity were used. A 15 residue overlapping peptide library representing the C-terminal half of hTf with an 11 amino acid overlap was prepared. This is essentially identical to the library used in a prior study (35) and the intact N-lobe of *M. catarrhalis* TbpB recognized an almost identical set of peptides (Segments 1-7, Table 3)

One cannot extrapolate the teaching of the specification to the scope of the claims because the claims as written are drawn to variants of SEQ ID NO:17 with undefined alterations of the 17 amino acid residues of SEQ ID NO:17 as well as undefined variants which comprise 17 plus 4 amino acids on n-terminus and 4 amino acids on carboxyl terminus of SEQ ID NO:17 and neither the specification nor the art of record define which amino acid residues are critical to the raising of antibodies that are specific for SEQ ID NO:17 or which will be recognized by antibodies from *M. catarrhalis*.

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With respect to claim 1 (b) , although conservative substitutions increase the chance of having less effect on the activity of the protein, it is unpredictable which amino acid at a certain position could be substituted even by conservative substitution. For example, Straub P et al, 1993, J Biol Chem 268(29): 21997-20003, teach that conservative substitutions of valine for glycine at positions 111 and 117 of cytochrome P450 2C2 result in about 50- and 7-fold reduction of activity, respectively. Kouklis PD et al, 1993, J Cell Science, 106(pt 3): 919-28, teach that a single exchange of glycine 450 of the intermediate filament protein vimentin with valine strongly interferes with the normal assembly of the intermediate filaments. Additionally, the art specifically teaches proteins with replacement of single amino acid residues may lead to both structural and functional changes in biological activity and immunological recognition. For example, Jobling et al. (Mol. Microbiol. 1991, 5(7): 1755-67 teaches a panel of single amino acid substitutions by oligonucleotide directed mutagenesis in proteins and they differ in native conformation, immunological recognition, binding and toxicity, thus exemplifying the importance of structural components to both biological function and immunological recognition. Therefore, changes made to a polypeptide lead to unpredictable biological activity.

With respect to claim 1(c) as drawn to the effects of the added amino acid residues on the ability to bind transferrin at the indicated region, Bowie et al (Science, 1990, 257:1306-1310), teaches that an amino acid sequence encodes a message that determines the shape of a protein and determines the ability of said protein to fold into unique three-dimensional structures that allows them to function. Bowie further teaches that certain positions in the sequence are critical to the three dimensional structure/function relationship (p. 1306, cols 1 and 2). In addition, the sensitivity of binding proteins to alterations of even a single amino acid in a sequence is exemplified by Burgess et al (J of Cell Bio. 111:2129-2138, 1990) who teach that replacement of a single lysine residue at position 118 of acidic fibroblast growth factor by glutamic acid led to the substantial loss of heparin binding, receptor binding and biological activity of the protein.

Clearly, given the teaching of Burgess et al, and Bowie et al, it is clear that the structure of the binding protein is critical to the ability of the protein to bind. Given the art recognized exquisite specificity of protein binding/antibody binding, given the undefined nature of the added amino acid residues, it is not possible to predict what affect the change in conformation expected by that addition would have on the binding capabilities of SEQ ID NO:17 and in the absence of further guidance in the specification one would not know how to make the claimed invention without random experimentation and random experimentation is unpredictable.

With respect to claim 2 it is well established in the art that the formation of an intact antigen-binding site generally requires the association of the complete heavy and light chain variable regions of a given antibody, each of which consists of three CDRs which provide the majority of the contact residues for the binding of the antibody to its target epitope. The amino acid sequences and conformations of

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each of the heavy and light chain CDRs are critical in maintaining the antigen binding specificity and affinity which is characteristic of the parent immunoglobulin. It is expected that all of the heavy and light chain CDRs in their proper order and in the context of framework sequences which maintain their required conformation, are required in order to produce a protein having antigen-binding function and that proper association of heavy and light chain variable regions is required in order to form functional antigen binding sites. Even minor changes in the amino acid sequences of the heavy and light variable regions, particularly in the CDRs, may dramatically affect antigen-binding function as evidenced by Rudikoff et al (Proc Natl Acad Sci USA 1982 Vol 79 page 1979). Rudikoff et al. teach that the alteration of a single amino acid in the CDR of a phosphocholine-binding myeloma protein resulted in the loss of antigen-binding function. Therefore, given that the claimed SEQ ID NO:17 is a 14mer, it does not appear possible that the 14mer comprises all of the CDRs and framework sequences required for an antigen binding antibody and one would not know how to make the claimed invention so that it would function as claimed.

With respect to claim 4, transferrin binding protein B (TbpB) from a human Gram negative bacteria, the specification clearly indicates that TbpB, SEQ.ID.NO:17 from *M. catarrhalis* has no consensus sequence with other gram negative bacterial TbpB (see Table 3 or 4). Therefore, the TbpB is specific for each bacterial strain and it would not appear possible to use the invention as claimed as claimed with any gram negative bacterial pathogen other than *M. catarrhalis*.

Further, there is no teaching in the specification of whether or not the epitopes are linear or comprise 3-dimensional structures. In particular, Greenspan et al (Nature Biotechnology, 1999, 7:936-937) teaches that defining epitopes is not as easy as it seems. Even when the epitope is defined, in terms of the spatial organization of residues making contact with ligand, then a structural characterization of the molecular interface for binding is necessary to define the boundaries of the epitope (page 937, 2nd column).

The specification provides insufficient guidance with regard to these issues and provides no working examples which would provide guidance to one skilled in the art and no evidence has been provided which would allow one of skill in the art to predict that the invention as broadly claimed would function as claimed with a reasonable expectation of success. For the above reasons, it appears that undue experimentation would be required to practice the claimed invention.

Some of Applicant's arguments drawn to previous rejection of the claims are relevant to the instant rejection.

Applicant argues that independent claim 1 has been amended to recite specific isolated polypeptides having particular amino sequences and polypeptides of claim 1 are suitable for generating antibodies under various conditions, including in vivo conditions. The specification describes compositions (carriers, adjuvants, etc.) that include such polypeptides and teaches that the composition can be used to induce an immune system, e.g., to produce antibodies which will serve to vaccinate the host against a Gram negative bacterial infection without causing the disease itself.

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The argument has been considered but has not been found persuasive because the claim as amended recites not only isolated polypeptide consisting of the amino acid sequence but also variants of SEQ.ID.NO:17. Further, claim 2 recites the polypeptide is an antibody. Therefore, the rejection of record as discussed above applies to the amended claims.

Remarks

7. No claims are allowed

Conclusion

8. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP ' 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for response to this final action is set to expire THREE MONTHS from the date of this action. In the event a first response is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event will the statutory period for response expire later than SIX MONTHS from the date of this final action.

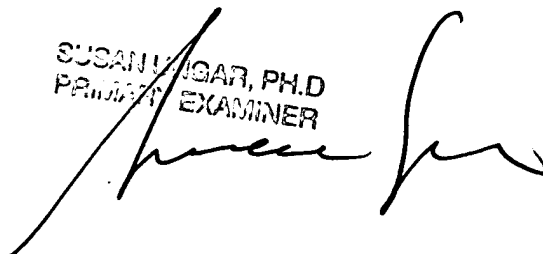
9. Papers related to this application may be submitted to Group 1600, AU 1645 by facsimile transmission. Papers should be transmitted via the PTO Fax Center, which receives transmissions 24 hours a day and 7 days a week. The transmission of such papers by facsimile must conform to the notice published in the Official Gazette, 1096 OG 30, November 15, 1989. The Right Fax number is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PMR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PMR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PMR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Padma Baskar Ph.D., whose telephone number is ((571) 272-0853. A message may be left on the Examiner's voice mail system. The Examiner can normally be reached on Monday to Friday from 6.30 a.m. to 4.00 P.M except First Friday of each bi-week.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jeffrey Siew can be reached on (571) 272-0787.


Padma Baskar Ph.D.


SUSAN NAGAR, PH.D.
PRINCIPAL EXAMINER